

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:48:26 ; Search time 100 Seconds
(without alignments)
210.958 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 CAGCAGCAGAGTCTTCATCAT 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 377018

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	10	US-09-944-326-4
2	14.8	70.5	21	10	US-09-944-326-1
3	14.8	70.5	21	10	US-09-944-326-2
C 4	14.8	70.5	31	9	US-10-196-107A-35
C 5	14.8	70.5	31	10	US-09-374-671-35
C 6	14.2	67.6	22	9	US-10-006-856A-163
C 7	14.2	67.6	22	9	US-10-006-818A-163
C 8	14.2	67.6	22	9	US-10-015-393A-163
C 9	14.2	67.6	26	9	US-10-006-856A-164
C 10	14.2	67.6	26	9	US-10-006-818A-164
C 11	14.2	67.6	26	9	US-10-015-393A-164
C 12	13.8	65.7	28	9	US-09-864-364-3
C 13	13.8	65.7	37	10	US-10-196-107A-54
C 14	13.8	65.7	37	10	US-09-374-671-54
C 15	13.6	64.8	24	10	US-09-939-709-3
C 16	13.6	64.8	49	9	US-09-805-353-19
C 17	13.6	64.8	50	9	US-09-992-598-312
C 18	13.6	64.8	50	9	US-09-989-293A-312
C 19	13.6	64.8	50	9	US-09-989-735-312

20 13.6 64.8 50 9 US-09-990-444-312 Sequence 312, App
21 13.6 64.8 50 9 US-09-989-730-312 Sequence 312, App
22 13.6 64.8 50 9 US-09-990-436-312 Sequence 312, App
23 13.6 64.8 50 9 US-09-991-181-312 Sequence 312, App
24 13.6 64.8 50 9 US-09-993-687-312 Sequence 312, App
25 13.6 64.8 50 9 US-09-989-734-312 Sequence 312, App
26 13.6 64.8 50 9 US-09-997-653-312 Sequence 312, App
27 13.6 64.8 50 9 US-09-993-667-312 Sequence 312, App
28 13.6 64.8 50 9 US-09-990-438-312 Sequence 312, App
29 13.6 64.8 50 9 US-09-990-562-312 Sequence 312, App
30 13.6 64.8 50 9 US-09-997-428-312 Sequence 312, App
31 13.6 64.8 50 9 US-09-997-666-312 Sequence 312, App
32 13.6 64.8 50 9 US-09-990-711-312 Sequence 312, App
33 13.6 64.8 50 9 US-09-989-726-312 Sequence 312, App
34 13.6 64.8 50 9 US-09-990-437-312 Sequence 312, App
35 13.6 64.8 50 9 US-09-998-156-312 Sequence 312, App
36 13.6 64.8 50 9 US-09-991-157-312 Sequence 312, App
37 13.6 64.8 50 9 US-09-991-172-312 Sequence 312, App
38 13.6 64.8 50 9 US-09-997-514-312 Sequence 312, App
39 13.6 64.8 50 9 US-09-997-573-312 Sequence 312, App
40 13.6 64.8 50 9 US-09-990-443-312 Sequence 312, App
41 13.6 64.8 50 9 US-09-990-726-312 Sequence 312, App
42 13.6 64.8 50 9 US-09-997-559-312 Sequence 312, App
43 13.6 64.8 50 9 US-09-997-601-312 Sequence 312, App
44 13.6 64.8 50 9 US-09-989-729A-312 Sequence 312, App
45 13.6 64.8 50 9 US-09-990-440-312 Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-944-326-4
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944.326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCAGCAGAGTCTTCATCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 2
US-09-944-326-1
; Sequence 1, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin

```

; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-1

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Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CAGCAGCAGAGTCTTCAT 18
||||| ||| |||||
Db 4 CAGCAGGAGATCTTCAT 21

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RESULT 3
US-09-944-326-2
; Sequence 2, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: mismatch control
US-09-944-326-2

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Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CAGCAGCAGAGTCTTCAT 18
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Db 4 CAGCAGGAGATCTTCAT 21

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RESULT 4
US-10-196-107A-35/c
; Sequence 35, Application US/10196107A
; Publication No. US20030049691A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Konieczny, Andrzej

```

```

; Bizindauskas, Christine B.
; Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/196,107A
; FILING DATE: 16-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/374,671
; FILING DATE: 1999-AUG-16
; APPLICATION NUMBER: US 08/491,861
; FILING DATE: 1995-OCT-27
; APPLICATION NUMBER: PCT/US93/12468
; FILING DATE: 1993-DEC-30
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22
; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 742-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-196-107A-35

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Query Match 70.5%; Score 14.8; DB 9; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 AGCAGCAGAGTCTTCATC 19
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Db 24 AGGAGCAGGCTTCATC 7

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RESULT 5
US-09-374-671-35/c
; Sequence 35, Application US/09374671
; Patent No. US2002012963A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Konieczny, Andrzej
; APPLICANT: Bizindauskas, Christine B.
; APPLICANT: Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston

```

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-374-671-35

Query Match 70.5%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AGCAGCAGAGTCTTTCATC 19
Db 24 AGGAGCAGGGTCTTTCATC 7

RESULT 6
US-10-006-856A-163/c
Sequence 163, Application US/10006856A
Publication No. US2003004841A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C14
CURRENT APPLICATION NUMBER: US/10/006,856A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 163
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-163

Query Match 67.6%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGTCTTTCATC 19
Db 22 CAGGACAGGGTCTTTCATC 4

RESULT 7
US-10-006-818A-163/c
Sequence 163, Application US/10006818A
Publication No. US20030054406A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C4
CURRENT APPLICATION NUMBER: US/10/006,818A
CURRENT FILING DATE: 2001-12-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 163
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-163

Query Match 67.6%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGTCTTTCATC 19
Db 22 CAGGACAGGGTCTTTCATC 4

RESULT 8
US-10-015-393A-163/c
Sequence 163, Application US/10015393A
Publication No. US20030069179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
US-10-006-856A-163

```
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PlC46
; CURRENT APPLICATION NUMBER: US/10/015.393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 163
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-015-393A-163
```

Query Match 67.6%; Score 14.2; DB 9; Length 22;

Best Local Similarity 84.2%; Pred. No. 9.4e+02; Mismatches 0; Gaps 0; Indels 0;

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Oy 1 CAGCAGCAGAGTCTTCATC 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 9

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US-10-006-856A-164/c
; Sequence 164, Application US/10006856A
; Publication No. US20030044841A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC14
; CURRENT APPLICATION NUMBER: US/10/006.856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-006-856A-164
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Query Match 67.6%; Score 14.2; DB 9; Length 26;

Best Local Similarity 84.2%; Pred. No. 9.6e+02; Mismatches 0; Gaps 0; Indels 0;

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Oy 1 CAGCAGCAGAGTCTTCATC 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 10

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US-10-006-818A-164/c
; Sequence 164, Application US/10006818A
; Publication No. US20030054406A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

```
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC4
; CURRENT APPLICATION NUMBER: US/10/006.818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-006-818A-164
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Query Match 67.6%; Score 14.2; DB 9; Length 26;

Best Local Similarity 84.2%; Pred. No. 9.6e+02; Mismatches 0; Gaps 0; Indels 0;

```
Oy 1 CAGCAGCAGAGTCTTCATC 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 11

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US-10-015-393A-164/c
; Sequence 164, Application US/10015393A
; Publication No. US20030069179A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC46
; CURRENT APPLICATION NUMBER: US/10/015.393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-015-393A-164
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Query Match 67.6%; Score 14.2; DB 9; Length 26;

Best Local Similarity 84.2%; Pred. No. 9.6e+02; Mismatches 0; Gaps 0; Indels 0;

QY 1 CAGCAGCAGGCTTCATC 19
||| | ||| ||||| |||
Db 22 CAGGACAGGCTTCATC 4

RESULT 12
US-09-864-364-3/c
; Sequence 3, Application US/09864364
; Publication No. US20030005470A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAISEIYAKU KABUSIKIGAISYA
; TITLE OF INVENTION: NO. US20030005470A1-Human Animal Exhibiting Bone Metastasis Of Tu
; FILE REFERENCE: PH-1182US
; CURRENT APPLICATION NUMBER: US/09/864,364
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: JP 2001-140538
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IL-11 primer
US-09-864-364-3

Query Match 65.7%; Score 13.8; DB 9; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CAGCAGGCTTCATCA 20
||||| ||||| ||| |||
Db 25 CAGCCGAGCTTCAGCA 9

RESULT 13
US-10-196-107A-54/c
; Sequence 54, Application US/10196107A
; Publication No. US20030049691A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; Konieczny, Andrzej
; Bizindaukas, Christine B.
; Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/196,107A
; FILING DATE: 16-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/374,671
; FILING DATE: 1999-AUG-16
; APPLICATION NUMBER: US 08/491,861
; FILING DATE: 1995-OCT-27
; APPLICATION NUMBER: PCT/US93/12468
; FILING DATE: 1993-DEC-30
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22

; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-196-107A-54

Query Match 65.7%; Score 13.8; DB 9; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGGCTTCAT 18
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Db 30 AGGACGAGGCTTCAT 14

RESULT 14
US-09-374-671-54/c
; Sequence 54, Application US/09374671
; Patent No. US20020012963A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; Konieczny, Andrzej
; APPLICANT: Bizindaukas, Christine B.
; APPLICANT: Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic proteins and peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374,671
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/491,861
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

US-09-374-671-54

Query Match 65.7%; Score 13.8; DB 10; Length 37;
 Best Local Similarity 88.2%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCAT 18
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 Db 30 AGGAGCAGGGTCTTCAT 14

RESULT 15

US-09-939-709-3
 ; Sequence 3, Application US/099393709
 ; Patent No. US2002007273A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARON, Roland E.
 ; APPLICANT: SIMS, Natalie
 ; APPLICANT: SABATAKOS, Georgios
 ; APPLICANT: NESTLER, Eric
 ; APPLICANT: CHEN, Jingshan
 ; APPLICANT: KELZ, Max
 ; TITLE OF INVENTION: Methods of Using Agents that Modulate Bone Formation and Inhibit
 ; FILE REFERENCE: Adipogenesis
 ; FILE REFERENCE: 044574-5045-US
 ; CURRENT APPLICATION NUMBER: US/09/939,709
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: US 60/228,450
 ; PRIOR FILING DATE: 2000-08-29
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide: SV40 primer
 US-09-939-709-3

Query Match 64.8%; Score 13.6; DB 10; Length 24;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCA 20
 ||||| || |||||
 Db 3 CAGCAGTAGCCTCATCA 22

Search completed: April 18, 2003, 08:58:39
 Job time : 108 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:44:37 ; Search time 1679 Seconds
(without alignments)
202.564 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcaggtcttcattcatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	70.5	46	9	AA916352 oh80ell.s
2	14.6	69.5	44	14	W25663 zc64e08.r1
3	14	66.7	50	17	BH861678 SALK_0877
4	13	61.9	21	17	AZ802584 2M0061105
5	13	61.9	43	9	AA973632 oc48b04.s
6	12.8	61.0	46	9	AL649065 AL649065

7	12.8	61.0	50	9	AA107924
8	12.8	61.0	50	9	AA107925
9	12.8	61.0	50	9	AA107928
10	12.8	61.0	50	9	AA107929
c 11	12.6	60.0	39	17	AL760945
c 12	12.6	60.0	43	9	AA1766391
c 13	12.6	60.0	46	9	AA561123
c 14	12.6	60.0	40	9	AA561123 v14c01.r
c 15	12.6	60.0	50	9	AA105963
c 16	12.6	60.0	50	9	AA105967
c 17	12.6	60.0	50	9	AA105968
c 18	12.6	60.0	50	9	AA105972
c 19	12.4	59.0	37	17	AZ797149
c 20	12.2	58.1	35	17	AZ332831
c 21	12.2	58.1	43	17	AZ610505
c 22	12.2	58.1	46	9	AA109083
c 23	12.2	58.1	49	9	AA052336
c 24	12.2	58.1	49	9	AA864073
c 25	12.2	58.1	50	9	AA104442
c 26	12	57.1	33	17	AZ305164
c 27	12	57.1	33	17	AZ318599
c 28	12	57.1	34	9	AA116347
c 29	12	57.1	34	13	BI246596
c 30	12	57.1	46	14	H92446
c 31	12	57.1	46	14	T74174
c 32	12	57.1	47	17	AZ772648
c 33	12	57.1	49	9	AI197165
c 34	12	57.1	49	17	AQ025388
c 35	12	57.1	50	9	AA103332
c 36	12	57.1	50	9	AA103352
c 37	12	57.1	50	9	AA107277
c 38	11.8	56.2	21	17	AZ848076
c 39	11.8	56.2	26	17	AA600116
c 40	11.8	56.2	37	9	AA079070
c 41	11.8	56.2	38	17	AZ815373
c 42	11.8	56.2	50	9	AA105966
c 43	11.8	56.2	50	9	AA106538
c 44	11.6	55.2	40	9	AA725970
c 45	11.6	55.2	41	17	AL760282

ALIGNMENTS

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RESULT 1
AA916352 46 bp mRNA linear EST 14-APR-1998
LOCUS oh80ell.s1 NCI-CGAP_C08 Homo sapiens cDNA clone IMAGE:1473356 3'
DEFINITION similar to TR:Q15347 Q15347 RAG4. [1] ; mRNA sequence.
ACCESSION AA916352
VERSION AA916352.1 GI:3055744
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Cloning Distribution: NCI-CGAP University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
```


QY 3 GCAGCAGAGTCTTC 16
 Db 41 GCAGCAGAGTCTTC 28

RESULT 4
 LOCUS AZ802584 21 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M061105R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0061105 R, DNA sequence.
 ACCESSION AZ802584
 VERSION AZ802584.1 GI:12954907
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Stokes,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0061 row: 1 column: 05
 Seq primer: CACACGAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

Location/Qualifiers
 1.. 21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0061105"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 8 a 7 c 3 g

BASE COUNT

ORIGIN

Query Match 61.9%; Score 13; DB 17; Length 21;
 Best Local Similarity 76.2%; Pred. No. 3e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 1 CAGCAGCAGCATACATCAT 21

RESULT 5
 LOCUS AA973632 43 bp mRNA linear EST 17-JUN-1998
 DEFINITION o048b04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569391 3',
 similar to SW_XPE_CERAE P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ;,
 mRNA sequence.
 ACCESSION AA973632
 VERSION AA973632.1 GI:3148812
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 703 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1569391"
 /clone_lib="NCI_CGAP_Lu5"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: p7T73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 neuroendocrine lung carcinoid, and was then primed with a
 Not I - oligo(dT) primer. Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library is normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo."
 15 a 13 c 6 g 9 t

BASE COUNT

ORIGIN

Query Match 61.9%; Score 13; DB 9; Length 43;
 Best Local Similarity 76.2%; Pred. No. 4.4e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 1 CAACAATAGAGTCTTCACCAT 21

BASE COUNT

ORIGIN

Query Match 61.9%; Score 13; DB 9; Length 43;
 Best Local Similarity 76.2%; Pred. No. 4.4e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 6
 LOCUS AL649065 46 bp mRNA linear EST 13-DEC-2001
 DEFINITION AL649065 XCC-gastrula Silurana tropicalis cDNA clone IGas034101 5',
 mRNA sequence.
 ACCESSION AL649065
 VERSION AL649065.1 GI:17658059

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KEYWORDS
SOURCE      western clawed frog.
ORGANISM    Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1 (bases 1 to 46)
AUTHORS     Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
TITLE       Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL     Unpublished (2001)
COMMENT     Contact: Huckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: tropesanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: Tgas034101.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES
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        /dev_stage="gastrula (stages 10.5-13 mixed)"
        /lab_host="Escherichia coli XL1-blue"
        /note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA
        was oligo dT primed from 5ug of poly A+ RNA from stages
        10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
        into PCS107 with EcoRI at the 5' end and NotI at the 3'
        end."
BASE COUNT   10 a   14 c   11 g   11 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 46;
Best Local Similarity 87.5%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCAGAGTCTTCATCAT 21
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Db 21 GCCGCGTTCATCAT 36

RESULT 7
AUI07924
LOCUS       AUI07924 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   HRC02185, mRNA sequence.
ACCESSION   AUI07924
VERSION     AUI07924.1 GI:13557446
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
            Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
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                /clone_lib="Sugano Homo sapiens cDNA library"
                /note="Differential display comparison of untreated and
                dimethylfumarate treated U937 cells"
BASE COUNT   10 a   15 c   19 g   6 t
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Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||| ||||| |||||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 9
AUI07928
LOCUS       AUI07928 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   ZRV62248, mRNA sequence.
ACCESSION   AUI07928

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Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||| ||||| |||||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 8
AUI07925
LOCUS       AUI07925 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   HSI06916, mRNA sequence.
ACCESSION   AUI07925
VERSION     AUI07925.1 GI:13557447
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                /note="Differential display comparison of untreated and
                dimethylfumarate treated U937 cells"
BASE COUNT   10 a   15 c   19 g   6 t
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Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||| ||||| |||||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 9
AUI07928
LOCUS       AUI07928 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   ZRV62248, mRNA sequence.
ACCESSION   AUI07928

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VERSION      AU107928.1  GI:13557450
KEYWORDS     EST.
SOURCE       Homo sapiens
ORGANISM     Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
              , H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
              , Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
              , S. Construction and characterization of a full length-enriched and
              a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES     source
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              /db_xref="taxon:9606"
              /clone_lib="Sugano Homo sapiens cDNA library"
              /note="Differential display comparison of untreated and
              dlmethyulfumarate treated u937 cells"
BASE COUNT   10 a 15 c 20 g 5 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AGCAGCAGAGTCTTCA 17
      |||||
Db   29 AGCAGCAGAGTCCGCA 44

RESULT 11
AL760945/c
LOCUS      AL760945          39 bp      DNA      linear      GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-204B10-014508,
              genomic survey sequence.
ACCESSION  AL760945
VERSION     AL760945.1  GI:21501350
KEYWORDS    GSS
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1
AUTHORS      Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
              and Weissshaar, B.
TITLE        A pipeline for automated high-throughput generation of FSTs
              (flanking sequence tags) from Arabidopsis thaliana T-DNA
              transformed lines
              Unpublished
JOURNAL
REFERENCE    2
AUTHORS      Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.
              A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
              for flanking sequence tag based reverse genetics
              Unpublished
JOURNAL
REFERENCE    3 (bases 1 to 39)
AUTHORS      Rosso, M., Li, Y., Strizhov, N. and Weissshaar, B.
              Direct Submission
TITLE        Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
              This sequence is recovered from the left border of the T-DNA. It
              indicates an insertion within the locus defined by clone t10j7. The
              sequences are generated at the MPI for Plant Breeding Research in
              the context of the GABI-Kat project. GABI-Kat is part of the German
              Plant Genomics program designated 'GABI'. Information on line
              availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES     Location/Qualifiers
              1..39
              /organism="Arabidopsis thaliana"
              /strain="Columbia 0"
              /db_xref="taxon:3702"
              /clone_lib="GK-204B10-014508"
              /note="PCR was performed on DNA from Arabidopsis thaliana
              plants (T1) which were transformed with the T-DNA from
              vector pAC161. The lines contain one or more T-DNA
              insertions. The DNA fragment(s) resulting from the PCR
              were directly sequenced to determine the genomic sequence
              flanking the insertion. Sequences displaying significant
              similarity to the A. thaliana nuclear genome sequence were
              processed for submission. T-DNA derived sequences were
              removed"
BASE COUNT   10 a 12 c 10 g 7 t
ORIGIN

```

```

Query Match      60.0%; Score 12.6; DB 17; Length 39;
Best Local Similarity 78.9%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2  AGCAGCAGAGTCTTCATCA 20
    ||| ||||| ||| ||
Db   38  AGCGCAGAGTGTCTTCCA 20

RESULT 12
A1766391/c
LOCUS      A1766391      43 bp      mRNA      linear      EST 20-DEC-1999
DEFINITION wh61d04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385223 3'
            similar to SW:COX2_HUMAN P00403 CYTOCHROME C OXIDASE POLYPEPTIDE II
            ; mRNA sequence.
ACCESSION  A1766391
VERSION     A1766391.1  GI:5232900
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1  (bases 1 to 43)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/brpr/image/image.html

Trace considered overall poor quality
Insert Length: 641 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 1.
FEATURES    source
            Location/Qualifiers
                1..43
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2385223"
                /clone.lib="NCI_CGAP_Kid11"
                /lab_host="DH10B"
                /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                prepared, and ss circles were made in vitro. Following HAP
                purification, this DNA was used as tracer in a subtractive
                hybridization reaction. The driver was PCR-amplified cDNAs
                from a pool of 5,000 clones made from the same library
                (cloneIds 1323376-1323911, 1456007-1456775, and
                1500552-1502855). Subtraction by Bento Soares and M.
                Fatima Bonaldo."
BASE COUNT   10 a  5 c  21 g      7 t
ORIGIN
Query Match      60.0%; Score 12.6; DB 9; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1  CAGCAGCAGAGTCTTCATC 19
    ||| ||| ||| |||||
Db   32  CATCATCATAGCTTCATC 14

RESULT 13
AA561123/c
LOCUS      AA561123      46 bp      mRNA      linear      EST 18-AUG-1997
DEFINITION v141c01.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:974784 5' similar to TR:G972037 G972037 SUCCINATE
            DEHYDROGENASE ;, mRNA sequence.
ACCESSION  AA561123
VERSION     AA561123.1  GI:2332588
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1  (bases 1 to 46)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HHMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine#p
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:555512
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev1 Et from Amersham
            High quality sequence stop: 1.
FEATURES    source
            Location/Qualifiers
                1..46
                /organism="Mus musculus"
                /strain="C57BL/6"
                /db_xref="taxon:10090"
                /clone="IMAGE:974784"
                /clone.lib="Stratagene mouse skin (#937313)"
                /sex="females"
                /tissue_type="whole skin"
                /dev_stage="11 weeks old"
                /lab_host="SOLR (kanamycin resistant)"
                /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
                dt. Whole skin from 11 week old C57BL/6 female mice.
                Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5',
                adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor
                sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT   11 a  11 c  15 g      9 t
ORIGIN
Query Match      60.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 78.9%; Pred. No. 6.9e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1  CAGCAGCAGAGTCTTCATC 19
    |||| |||| ||| |||
Db   46  CAGCATCATGATTCGAGC 28

RESULT 14
AUI05963/c
LOCUS      AUI05963      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION AUI05963 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            COLF6356, mRNA sequence.
ACCESSION  AUI05963
VERSION     AUI05963.1  GI:13555484
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF6356"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 11 a 14 c 13 g 12 t
ORIGIN

Query Match 60.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| | | | | |
Db 21 AGCAGCAGAAATGTTCTGCA 3

RESULT 15
AUI05967/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI05967 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC05018, mRNA sequence.
ACCESSION AUI05967
VERSION AUI05967.1 GI:13555488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC05018"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 12 a 15 c 11 g 12 t
ORIGIN
Query Match 60.0%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| | | | | |
Db 48 AGCAGCAGAAATGTTCTGCA 30

Search completed: April 18, 2003, 08:55:26
Job time : 1691 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 05:56:34 ; Search time 233 Seconds
(without alignments)
202.970 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21
Sequence: 1 cagcagcagatcttcatcat 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94226	Human testostosterone
2	17.8	84.8	50	AAAX24790	Interleukin-18 bin
3	16.2	77.1	32	AAAX09140	Gos-2 promoter gen
4	16.2	77.1	50	AAAX11024	Human mature inter
5	15.2	72.4	22	AAAS15291	Mouse IL-12 p40 #1
6	15.2	72.4	21	AAAZ96146	Polynucleotide seq
7	14.8	70.5	21	AAAZ94223	Murine testosteron
8	14.8	70.5	21	AAA94224	Murine testosteron
9	14.8	70.5	27	AAH40683	SNP specific SNPE

c 10	14.8	70.5	30	20	AAZ12445	PCR primer used to
c 11	14.8	70.5	31	15	AAQ69972	5'sense leader ex
c 12	14.6	69.5	24	24	ABL61345	Naja naja atra sho
c 13	14.6	69.5	33	24	ABK49118	Human transcriptio
c 14	14.6	69.5	34	22	AAH79384	Plasmolemma regula
c 15	14.6	69.5	44	20	AAH06964	Bacillus lichenifo
c 16	14.2	67.6	20	20	AAZ31857	PCR primer for hum
c 17	14.2	67.6	20	24	ABK69555	Rat phosphorylase
c 18	14.2	67.6	22	21	AAK58494	Human PRO1283 (UNQ
c 19	14.2	67.6	22	21	AAA37208	Human PRO1283 forw
c 20	14.2	67.6	22	22	AAF54314	Primer #40 used in
c 21	14.2	67.6	24	20	AAH08676	Oligonucleotide de
c 22	14.2	67.6	24	22	AAH73404	Grand fir monoterp
c 23	14.2	67.6	26	21	AAK58495	Human PRO1283 (UNQ
c 24	14.2	67.6	26	21	AAA37209	Human PRO1283 forw
c 25	14.2	67.6	26	22	AAF54315	Primer #41 used in
c 26	14.2	67.6	30	20	AAH19511	Human lipocalin ho
c 27	14.2	67.6	34	18	AAH86354	Lambda primer 3.
c 28	13.8	65.7	18	21	AAZ57675	Human G-alpha-12 a
c 29	13.8	65.7	28	24	ABK14351	Human interleukin-
c 30	13.8	65.7	30	22	AAF28287	Oligonucleotide 5'
c 31	13.8	65.7	31	14	AAQ47780	PCR primer Lam B8
c 32	13.8	65.7	36	22	AAF56649	Human interleukin-
c 33	13.8	65.7	36	22	AAF56654	Human interleukin-
c 34	13.8	65.7	36	22	AAF56656	IL-11-IgG1-Fc dire
c 35	13.8	65.7	36	22	AAF56658	IL-11-IgG4-Fc dire
c 36	13.8	65.7	41	22	AAF28289	Modified gcc donor
c 37	13.8	65.7	50	22	AAZ43508	Corneodesmosin sin
c 38	13.6	64.8	20	20	AAH95224	PCR primer used to
c 39	13.6	64.8	20	22	AAZ45666	Human PARP-1 anti
c 40	13.6	64.8	23	21	AAH89796	3' RT-PCR primer u
c 41	13.6	64.8	24	24	ABK10729	SV40 RT-PCR primer
c 42	13.6	64.8	27	14	AAO40995	Annealing oligonuc
c 43	13.6	64.8	32	20	AAZ25040	Cyclin-dependent k
c 44	13.6	64.8	39	16	AAH80249	Chimeric rat/human
c 45	13.6	64.8	40	17	AAH70687	Fibrin clot bindin

ALIGNMENTS

RESULT 1
AAA94226
ID AAA94226 standard; DNA; 21 BP.
XX
AC AAA94226;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human testostosterone-repressed prostate message-2 antisense oligo #2.
XX
KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US04875.
XX
PR 26-FEB-1999; 99US-0121726.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX
DR WPI; 2000-53132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene -

PS Claim 3; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the

CC human testosterone-repressed prostate message-2 (TRPM-2, also known as

CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to

CC promote the regression of tumours, and oligonucleotides directed

CC at human TRPM-2 can be used in the treatment of tumour cells expressing

CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and

CC some breast cancer cells. In addition to this, they also increase the

CC chemosensitivity of the cells, meaning that conventional chemotherapy is

CC more effective.

XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

SQL

Query Match 100.0%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21

DB 1 CAGCAGCAGAGCTTCATCAT 21

RESULT 2

AAAX24790/c

ID AAAX24790 standard; DNA; 50 BP.

XX

AC AAAX24790;

DT 21-JUN-1999 (first entry)

XX

DE Interleukin-18 binding protein splice variant IL-18Bpa PCR primer.

XX

KW Interleukin-18 binding protein; IL-18BP; IL-18Bpa; splice variant;

KW human; autoimmune disease; inflammation; diabetes; pancreatitis;

KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;

KW psoriasis; inflammatory bowel disease; multiple sclerosis;

KW ischemic heart disease; ischemic brain injury; gene therapy; PCR;

KW primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9909063-A1.

XX

PD 25-FEB-1999.

XX

PF 13-AUG-1998; 98WO-IL00379.

XX

PR 22-JUL-1998; 98IL-0125463.

PR 14-AUG-1997; 97IL-0121554.

PR 27-AUG-1997; 97IL-0121639.

PR 29-SEP-1997; 97IL-0121860.

PR 06-NOV-1997; 97IL-0122134.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Dinarello C, Kim SH, Novick D, Rubinstein M;

XX

DR WPI; 1999-180975/15.

XX

PT New interleukin-18 binding protein - useful for treating human

PT diseases, including autoimmune disease and inflammation

PS

PS Example 7; Page 39; 100pp; English.

XX

CC The present sequence is a reverse primer that was used with a

CC forward primer (see AAAX24754) in the PCR amplification of the coding

CC region of a cDNA clone (see AAAX24749) coding for human interleukin-18

CC binding protein splice variant IL-18Bpa (see AAW98004). The PCR

CC products were cut with XbaI and cloned into the XbaI site of the

CC pEF-BOS expression vector. IL-Bp18a was expressed in transfected

CC COS7 cells. The invention provides IL-18BP polypeptides capable of

CC binding IL-18 and/or modulating and/or blocking IL-18 activity.

CC These can be used to treat conditions requiring the protein

CC (claimed), such as autoimmune diseases, type 1 diabetes, rheumatoid

CC arthritis, graft rejections, inflammatory bowel disease, sepsis,

CC multiple sclerosis, ischemic heart diseases, ischemic brain injury,

CC chronic hepatitis, psoriasis, and chronic/acute pancreatitis.

XX

SQL

Query Match 84.8%; Score 17.8; DB 20; Length 50;

Best Local Similarity 90.5%; Pred. No. 99;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21

DB 42 CAGCAGCAGAGCTTCATCAT 22

RESULT 3

AAA09140

ID AAA09140 standard; DNA; 32 BP.

XX

AC AAA09140;

XX

DT 10-AUG-2000 (first entry)

XX

DE Gos-2 promoter gene-specific primer 1.

XX

KW maize; promoter; actin-2; enolase; Gos-2; L41; gene expression;

KW regulation; plant transformation; primer; ss.

XX

OS Zea mays.

XX

PN WO200020571-A2.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23081.

XX

PR 06-OCT-1998; 98US-0103294.

PR 05-NOV-1998; 98US-0107201.

XX

PA (PION-) PIONEER HI-BRED INT INC.

PA (AGER-) AGERI AGRIC GENETIC ENG RES INST.

XX

PI Barbour E, Meyer TE, Saad ME;

XX

DR WPI; 2000-303763/26.

XX

PT Novel maize promoters used for producing transgenic plants with

PT regulated expression of heterologous nucleotide sequences

XX

PS Example 1; Page 26; 48pp; English.

XX

CC Novel maize promoters (AAA09134-37) that drive expression of actin-2,

CC enolase, Gos-2 or L41, respectively, were isolated from genomic DNA

CC using PCR. The first round of PCR was performed on each DNA sample

CC using PCR. The first round of PCR was performed on each DNA sample with

CC Clontech primer AP1 (AAA09138) and a gene-specific primer 1

CC (AAA09139-42), in a second round of PCR using Clontech primer AP2

CC (AAA09143) and a gene-specific primer 2 (AAA09144-47). Clones were

CC sequenced for verification and then amplified with Clontech primer AP3

CC (AAA09148) and a gene-specific primer (AAA09149-52). The promoters are

CC used for regulating the expression of heterologous nucleotide sequences

CC to vary the phenotype of a plant, e.g. modifying fatty acid composition,

CC altering amino acid content and altering the pathogen defense system of

CC the plant. Plants comprising important commercial traits can be

CC generated.

XX

SQL

Sequence 32 BP; 8 A; 12 C; 6 G; 6 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 32;

Best Local Similarity 85.7%; Pred. No. 4.9e+02;


```
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
    ||||| ||||| ||| |||
Db 3 CAGCACCAGAGCTCTTCATCAT 23

RESULT 4
AA11024/c
ID AA11024 standard; DNA; 50 BP.
XX
AC AA11024;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human mature interleukin 18 binding protein coding sequence primer #2.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
XX
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torigoe K, Taniai M, Kurimoto M;
XX
DR WPI; 2000-237850/20.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 2; Page 22; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents a PCR
CC primer used to isolate the coding sequence for the human mature
CC interleukin 12 binding protein (AA11002).
XX
SQ Sequence 50 BP; 7 A; 11 C; 18 G; 14 T; 0 other;

Query Match 77.18; Score 16.2; DB 21; Length 50;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
    ||||| ||||| ||| |||
Db 44 CAGCAGCAGGGGTCTACCAT 24

RESULT 5
AAS15291
ID AAS15291 standard; DNA; 22 BP.
XX
AC AAS15291;
XX
DT 16-JAN-2002 (first entry)
XX
DE Mouse IL-12 p40 #1 PCR primer 662F.

Mouse; ss; PCR primer; neurotropic; neuroprotective; 662F;
antiflammatory; interleukin-lbeta; IL-1b; tumour necrosis factoralpha;
TNFalpha; macrophage inflammatory protein-lalpha; MIP-lalpha;
fractalkane; glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;
major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;
neurodegenerative disease; VitD3-24OHase; MCP-1; IL-10; IL-12 p40;
IFN-gamma; CD3 epsilon; CD4; IgG-1; Ig k; osteopontin.
Mus sp.
WO200175165-A2.
11-OCT-2001.
30-MAR-2001; 2001WO-US10247.
30-MAR-2000; 2000US-193847P.
(ELAN-) ELAN PHARM INC.
McConlogue LC, Games KD, Yednock TA, Hua T, Messersmith E, Bard F;
WPI; 2001-639367/73.
Selecting compounds useful for treating or preventing Alzheimer's
disease, from their ability to reduce levels of specific disease
markers in animal models
Example 5; Page 23; 36pp; English.
The invention relates selecting compounds that reduce symptoms of
Alzheimer's disease using a non-human mammal that has been subjected to
cerebral ischaemia or lesion of a nerve so as to produce, in the
affected region, increased levels of specific markers of Alzheimer's
disease-associated inflammation. Test compounds are selected if they
reduce levels of these markers significantly, in the affected region,
relative to controls. The markers are interleukin-beta (IL-1b), tumour
necrosis factoralpha (TNFalpha), macrophage inflammatory protein-lalpha
(MIP-lalpha), glial fibrillar associated protein (GFAP), MHC (major
histocompatibility complex) Iialpha or II L, CD86, fractalkane or CX3CR1
(a receptor for fractalkane). The method is used to identify compounds
useful in treatment or prevention of Alzheimer's disease or other
neurodegenerative diseases that have an inflammatory component. The
method provides fast, accurate and quantitative drug screens.
The present sequence is a PCR primer used to determine the level of
a transcript for an efficacy marker in a transgenic mouse which
overexpresses APP and displays Alzheimer's like neuropathology. The
efficacy markers are VitD3-24OHase, MCP-1, IL-10, IL-12 p40, #1/#2,
IFN-gamma #1/#2, CD3 epsilon, CD4 #1/#2, IgG-1, Ig k (light chain).
Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match 72.48; Score 15.2; DB 22; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCA 20
    ||||| ||| ||||| |||
Db 2 CAGCACCAGCTCTTCATCA 21

RESULT 6
AAZ96146/c
ID AAZ96146 standard; DNA; 40 BP.
XX
AC AAZ96146;
XX
DT 10-APR-2000 (first entry)
XX
DE Polynucleotide sequence including binding site for BamHI.
XX
KW Ligand binding; restriction enzyme; nucleic acid determination;
```

```

KW XX pharmaceutical; BamHI; ss.
OS XX Synthetic.
PN XX WO9963077-A2.
PD XX
PF XX 09-DEC-1999.
PX XX 04-JUN-1999; 99WO-US12516.
XX XX
XX XX 04-JUN-1998; 98US-0087905.
XX XX 03-JUN-1999; 99US-0324672.
XX XX
XX XX (TWTE-) TM TECHNOLOGIES INC.
XX XX
XX XX Lane MJ, Benight AS, Faldasz BD;
XX XX WPI; 2000-116369/10.
XX XX
XX XX Modulating polynucleotide ligand binding site affinity using
XX XX determination of the flanking duplex sequences -
XX XX
XX XX Example 1; Page 45; 62pp; English.
XX XX
XX XX The invention provides a method for determining the sequence of
XX XX polynucleotide flanking regions that modulate ligand binding
XX XX characteristics of an adjacent binding site. The method comprises:
XX XX (i) providing a number of different duplex polynucleotides, each having
XX XX the same polynucleotide ligand binding site and a randomly synthesised
XX XX sequence flanking the binding site; (ii) exposing the duplex to a ligand
XX XX selective for the binding site; (iii) isolating the duplexes which bind or
XX XX do not bind the ligand; and (iv) determining the nucleotide composition
XX XX of the flanking duplex sequence by sequencing the duplex sequence
XX XX adjacent to the binding site. The invention is used to modulate the
XX XX ligand-binding characteristics of any nucleotide sequence. The invention
XX XX is less costly and more efficient than prior art techniques that moderate
XX XX ligand binding using small molecule pharmaceuticals. Sequences
XX XX AA295762-236170 represent polynucleotide sequences, including the binding
XX XX site for the restriction enzyme BamHI and used in the course of the
XX XX invention.
XX XX
XX XX Sequence 40 BP; 6 A; 5 C; 19 G; 10 T; 0 other;
XX XX
XX XX Query Match 72.4%; Score 15.2; DB 21; Length 40;
XX XX Best Local Similarity 85.0%; Pred. No. 1.4e+03;
XX XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX XX QY 1 CAGCAGCAGAGTCTTCATCA 20
XX XX ||||| ||| ||||| |||
XX XX Db 28 CAGCAACAGCGTCTTCCTCA 9
XX XX
XX XX RESULT 7
XX XX AAA94223
XX XX ID AAA94223 standard; DNA; 21 BP.
XX XX AC AAA94223;
XX XX
XX XX 12-JAN-2001 (first entry)
XX XX
XX XX Murine testosterone-repressed prostate message-2 antisense oligo #1.
XX XX
XX XX Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX XX sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX XX
XX XX Mus sp.
XX XX
XX XX Key Location/Qualifiers
XX XX modified_base 1
XX XX /*tag= a
XX XX /mod_base= OTHER
XX XX /note= "phosphorothioate backbone"
XX XX

```

```

PN XX WO200049937-A2.
XX XX
XX XX 31-AUG-2000.
XX XX
XX XX 25-FEB-2000; 2000WO-US04875.
XX XX
XX XX 26-FEB-1999; 99US-0121726.
XX XX
XX XX (UYBR-) UNIV BRITISH COLUMBIA.
XX XX
XX XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX XX WPI; 2000-533132/48.
XX XX
XX XX Treating prostatic tumors and renal cancers by antisense inhibition of
XX XX the testosterone-repressed prostate messenger-2 gene -
XX XX
XX XX Example 1; Page 35; 38pp; English.
XX XX
XX XX The present sequence is an antisense oligonucleotide directed at the
XX XX murine testosterone-repressed prostate message-2 (TRPM-2), also known as
XX XX clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX XX promote the regression of tumours in mice, and oligonucleotides directed
XX XX at human TRPM-2 can be used in the treatment of tumour cells expressing
XX XX the TRPM-2 gene. These include prostate cancer, renal cell cancer and
XX XX some breast cancer cells. In addition to this, they also increase the
XX XX chemosensitivity of the cells, meaning that conventional chemotherapy is
XX XX more effective.
XX XX
XX XX Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
XX XX
XX XX Query Match 70.5%; Score 14.8; DB 21; Length 21;
XX XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX XX QY 1 CAGCAGCAGAGTCTTCAT 18
XX XX ||||| ||| ||||| |||
XX XX Db 4 CAGCAGGAGAAATCTTCAT 21
XX XX
XX XX RESULT 8
XX XX AAA94224
XX XX ID AAA94224 standard; DNA; 21 BP.
XX XX AC AAA94224;
XX XX
XX XX 12-JAN-2001 (first entry)
XX XX
XX XX Murine testosterone-repressed prostate message-2 antisense control.
XX XX
XX XX Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX XX sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX XX
XX XX Mus sp.
XX XX
XX XX WO200049937-A2.
XX XX
XX XX 31-AUG-2000.
XX XX
XX XX 25-FEB-2000; 2000WO-US04875.
XX XX
XX XX 26-FEB-1999; 99US-0121726.
XX XX
XX XX (UYBR-) UNIV BRITISH COLUMBIA.
XX XX
XX XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX XX WPI; 2000-533132/48.
XX XX
XX XX Treating prostatic tumors and renal cancers by antisense inhibition of
XX XX the testosterone-repressed prostate messenger-2 gene -
XX XX
XX XX Example 1; Page 35; 38pp; English.
XX XX

```

XX The present sequence is a mismatch control used with an antisense
CC oligonucleotide directed at the murine testosterone-repressed prostate
CC message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or
CC SGP-2). The antisense sequence was shown to promote the regression of
CC tumours in mice, and similar oligonucleotides directed at human TRPM-2
CC can be used in the treatment of tumour cells expressing the TRPM-2 gene.
CC These include prostate cancer, renal cell cancer and some breast cancer
CC cells. In addition to this, they also increase the chemosensitivity of
CC the cells, meaning that conventional chemotherapy is more effective.
XX
SQ Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 other;

Query Match 70.5%; Score 14.8; DB 21; Length 21;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCAT 18
||||||| |||||
Db 4 CAGCAGCAGAGTCTTCAT 21

RESULT 9
AAH40683/C
ID AAH40683 standard; DNA: 27 BP.
XX
AC AAH40683;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 3479.
XX
KW Single nucleotide polymorphism: SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia, diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample
XX
PS Claim 1; Page 67; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being

CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence.
XX
SQ Sequence 27 BP; 5 A; 8 C; 4 G; 9 T; 1 other;

Query Match 70.5%; Score 14.8; DB 22; Length 27;
Best Local Similarity 84.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| || |||||
Db 22 AGCAGCAGAGTCTTCATCA 4

RESULT 10
AAZ12445/C
ID AAZ12445 standard; DNA: 30 BP.
XX
AC AAZ12445;
XX
DT 08-OCT-1999 (first entry)
XX
DE PCR primer used to amplify ORF83 of Neisseria species.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea;
KW PCR primer; ss.
XX
OS Synthetic.
OS Neisseria sp.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI; 1999-327407/27.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT diagnosis, treatment and prevention of infection
XX
PS Disclosure; Page 489; 524pp; English.
XX
CC PCR primers AAZ12359-Z12531 were used to amplify various open reading
CC frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae. These
CC ORFs (AAZ11972-Z12358) encode antigenic proteins (AAZ38499-Y38944). The
CC antigenic proteins, their fragments, their nucleic acids and antibodies
CC are used for diagnosis, prevention (as vaccines) or treatment of
CC Neisseria infections, such as meningitis, septicaemia and gonorrhea.
CC Both organisms are closely related. Fragments of the nucleic acids are

CC useful as hybridisation probes and antisense reagents.

XX
SQ Sequence 30 BP; 7 A; 10 C; 7 G; 6 T; 0 other;
Query Match 70.5%; Score 14.8; DB 20; Length 30;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGGCTTCAT 18
DB 29 CAGCAGCAGGCTTCAT 12

RESULT 11
AAQ69972/c
ID AAQ69972 standard; cDNA; 31 BP.

XX
AC AAQ69972;
XX
DT 13-MAR-1995 (first entry)
XX
DE 5'sense leader ex oligo primer to amplify 5' end Can fi cDNA.

XX
KW Canis familiaris; protein allergen; dog dander; dog hair; allergy;
KW T cell response; stimulation; diagnosis; sensitivity; therapeutic;
KW agents; PCR; polymerase chain reaction; primer; amplification;
KW probe; hybridisation; partial cDNA; degenerate; ss.

XX
OS Synthetic.

XX
PN WO9416068-A.

XX
PD 21-JUL-1994.

XX
PF 30-DEC-1993; 93WO-US12468.

XX
PR 31-DEC-1992; 92US-0999712.

XX
PR 22-NOV-1993; 93US-0156549.

XX
PA (IMMU-) IMMULOGIC PHARM CORP.

XX
PI Bizinkauskas CB, Brauer AW, Konieczny A, Morgenstern JP;

XX
DR WPI; 1994-249215/30.

XX
PT DNA encoding dog dander allergenic peptide(s) Can f I and Can f
PT II - used in the diagnosis and treatment of sensitivity to dog
PT dander

XX
PS Example 2; Page 59; 124pp; English.

XX
CC AAQ69972 is a 5' primer corresponding to residues -26 to -20 of Canfi
CC (AAQ59987). It is used with AAQ69973 to amplify and sequence the 5' end
CC of the Can fi cDNA. Peptides of the invention have the ability to
CC induce a T cell response, which may include T cell stimulation or
CC T cell nonresponsiveness. Some have the ability to bind the dog
CC dander specific IgE of dog dander allergic subjects. These peptides
CC are useful in diagnosing sensitivity to dog dander. Other peptides
CC significantly reduce the ability to bind dog dander allergic IgE and
CC are thus useful as therapeutic agents. (See also AAQ69951-Q70006 and
CC AAQ59987-60018 - these include primers, and probes for isolation of
CC cDNA coding Can fi and fII allergens and peptides derived from the
CC sequences.)

XX
SQ Sequence 31 BP; 7 A; 13 C; 5 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 15; Length 31;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGGCTTCATC 19

DB 24 AGCAGCAGGCTTCATC 7

RESULT 12
ABL61345/c
ID ABL61345 standard; DNA; 24 BP.

XX
AC ABL61345;

XX
DT 13-SEP-2002 (first entry)

XX
DE Naja naja atra short chain neurotoxin-associated PCR primer #1.

XX
KW Chinese cobra; neurotoxin; cancer; PCR; primer; ss.

XX
OS Naja naja atra.

XX
PN CN1337404-A.

XX
PD 27-FEB-2002.

XX
PF 03-AUG-2000; 2000CN-0119561.

XX
PR 03-AUG-2000; 2000CN-0119561.

XX
PA (SHAN-) SHANGHAI BIOENGINEERING RES CENT CHINESE.

XX
PI Cai Q, Yang S, Gong Y;

XX
DR WPI; 2002-384228/42.

XX
PT Short-chain nervous cobra toxin, its preparation and use -

XX
PS Example 1; Page 11; 30pp; Chinese.

XX
CC This invention describes a novel cobra short chain neurotoxin, the
CC polynucleotide encoding the polypeptide and the method for producing the
CC polypeptide by means of recombination technology. The invention also
CC discloses the method for curing several diseases, such as cancer, by
CC using the cobra short chain neurotoxin, and a medicine composite
CC containing the cobra short chain neurotoxin. This sequence represents a
CC PCR primer used in the amplification of the short chain neurotoxin
CC described in the method of the invention.

XX
SQ Sequence 24 BP; 7 A; 5 C; 6 G; 6 T; 0 other;

Query Match 69.5%; Score 14.6; DB 24; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.5e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGGCTTCATCAT 21

DB 21 CAGCAACAGAGTTTCCATCTT 1

RESULT 13

ID ABR49118/c

XX ABR49118 standard; DNA; 33 BP.

XX
AC ABR49118;

XX
DT 02-JUL-2002 (first entry)

XX
DE Human transcription factor LCR-FI9.02 PCR primer #1.

XX
KW Human; ss; transcription factor; LCR-FI9.02; erythropathy; PCR; primer.

XX
OS Homo sapiens.

XX
PN WO200220583-A1.

XX
PD 14-MAR-2002.

XX
PF 25-JUN-2001; 2001WO-CN01053.

XX PR 28-JUN-2000; 2000CN-0116922.
XX PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
XX PT Mao Y, Xie X;
XX DR WPI; 2002-351761/38.
XX PT Homo transcription factor F19.02 and encoding polynucleotide, used in
XX PT treatment of erythropathy -
XX PS Example 4; Page 18; 38pp; Chinese.
XX CC The invention relates to an isolated polypeptide of human (HOMO)
XX CC transcription factor ICR-F19.02 the cDNA encoding it, and its fragment,
XX CC analogue or derivative. Also included are vectors expressing the protein,
XX CC a host cell comprising the vector, the isolation of modulators of the
XX CC protein and an anti-transcription factor ICR-F19.02 antibody. The protein
XX CC and nucleic acid are used in diagnosis and treatment of erythropathy.
XX CC The present sequence is a PCR primer used to clone the cDNA encoding
XX CC transcription factor ICR-F19.02.
XX SQ Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 other;
Query Match 69.5%; Score 14.6; DB 24; Length 33;
Best Local Similarity 81.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
||||||| ||| |||||
DB 27 CAGCAGCACCACCTGTCATCAT 7
RESULT 14
ID AAH79384/C
XX ID AAH79384 standard; DNA; 34 BP.
XX AC AAH79384;
XX DT 04-DEC-2001 (first entry)
XX DE Plasmolemma regulation function-contained protein 70 CDNA PCR primer #3.
XX KW Plasmolemma regulation function-contained protein 70; cancer; HIV;
XX KW infection; gene therapy; human; PCR primer; ss.
XX OS Homo sapiens.
XX PN CN1302889-A.
XX PD 11-JUL-2001.
XX PF 29-OCT-1999; 99CN-0119927.
XX PR 29-OCT-1999; 99CN-0119927.
XX PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2001-566050/64.
XX PT Polypeptide-human protein 70 containing plasmolemma regulation function
XX PT and polynucleotide for coding it -
XX PS Example 5; Page 15(Disclosure); 27pp; Chinese.
XX CC The present invention provides the protein and coding sequences of human
XX CC plasmolemma regulation function-contained protein 70. The sequences can
XX CC be used in the treatment of cancer and HIV infection. The present
XX CC sequence is a PCR primer for the coding sequence of the invention.

SQ Sequence 34 BP; 5 A; 9 C; 9 G; 11 T; 0 other;
Query Match 69.5%; Score 14.6; DB 22; Length 34;
Best Local Similarity 81.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
||||||| ||| |||||
DB 27 CAACAGAAGCGCCTTCATCAT 7
RESULT 15
ID AAX06964
XX ID AAX06964 standard; DNA; 44 BP.
XX AC AAX06964;
XX DT 10-MAY-1999 (first entry)
XX DE Bacillus licheniformis xyloglucanase primer Xyloglu.upper.PstI.
XX KW Xyloglucanase; detergent; PCR; primer; ss.
XX OS Synthetic.
XX OS Bacillus licheniformis.
XX PN WO9902663-A1.
XX PD 21-JAN-1999.
XX PF 01-JUL-1998; 98WO-DK00290.
XX PR 24-OCT-1997; 97DK-0001213.
XX PR 07-JUL-1997; 97DK-0000822.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Bjornvad ME, Jorgensen PL, Outtrup H, Schuelein M;
XX DR WPI; 1999-120866/10.
XX PT New enzyme preparation comprising a xyloglucanase with an activity
XX PT of 50 % at pH 7 - useful for improving the properties of cellulosic
XX PT fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and
XX PT linen fibres
XX PS Example 5; Page 60; 87pp; English.
XX CC Primers Xyloglu.upper.PstI and Xyloglu.lower.NotI (see AAX06965) were
XX CC used for the PCR amplification of Bacillus licheniformis ATCC 14580
XX CC xyloglucosidase DNA (see also AAX06949), using chromosomal DNA as
XX CC template. The primers incorporate PstI and NotI sites into the
XX CC amplified DNA. The PCR product was ligated into plasmid pMOL944, a
XX CC pUBI10 derivative containing elements making it propagatable in
XX CC Bacillus subtilis. The B. licheniformis xyloglucanase (see AAX06949)
XX CC was expressed in transformed B. subtilis PL2954 cells. The enzyme
XX CC is useful for improving the properties of cellulosic fabrics and in
XX CC detergent compositions.
XX SQ Sequence 44 BP; 7 A; 16 C; 12 G; 9 T; 0 other;
Query Match 69.5%; Score 14.6; DB 20; Length 44;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
||||||| ||| |||||
DB 12 CAGCAGCGCGCTTCATCAT 32
Search completed: April 18, 2003, 07:51:31
Job time : 239 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:47:42 ; Search time 52 Seconds
(without-alignments)
123.850 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcagagtttcattcat 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	73.3	45	1	US-07-885-689A-7
2	14.8	70.5	31	2	US-08-467-603-35
3	14.8	70.5	31	2	US-08-466-793-35
4	14.8	70.5	31	2	US-08-491-861A-35
5	14.6	69.5	44	4	US-09-110-959A-11
6	14.2	67.6	20	2	US-09-205-860-3
7	14.2	67.6	20	4	US-09-657-452A-163
8	14.2	67.6	24	4	US-09-360-545-57
9	14.2	67.6	30	3	US-09-130-663-10
10	14.2	67.6	30	3	US-09-432-335-10
11	14.2	67.6	30	4	US-09-254-023B-20
12	14.2	67.6	30	4	US-09-614-022-10
13	13.8	65.7	18	2	US-09-256-496-15
14	13.8	65.7	37	2	US-08-467-603-54
15	13.8	65.7	37	2	US-08-466-793-54
16	13.8	65.7	37	2	US-08-491-861A-54
17	13.6	64.8	20	4	US-09-517-467B-87
18	13.6	64.8	23	4	US-09-489-085A-6
19	13.6	64.8	27	6	5463174-1
20	13.4	63.8	20	4	US-09-657-452A-162
21	13.4	63.8	34	1	US-08-373-124A-27
22	13.4	63.8	34	1	US-08-435-628-27
23	13.2	62.9	18	2	US-09-205-860-28
24	13.2	62.9	24	4	US-09-442-099A-9
25	13.2	62.9	33	2	US-08-343-443B-100
26	13.2	62.9	38	3	US-09-130-663-26
27	13.2	62.9	38	3	US-09-432-335-26
Sequence 7, Appli					Sequence 7, Appli
Sequence 35, Appl					Sequence 35, Appl
Sequence 35, Appl					Sequence 35, Appl
Sequence 11, Appl					Sequence 11, Appl
Sequence 3, Appli					Sequence 3, Appli
Sequence 163, App					Sequence 163, App
Sequence 57, Appl					Sequence 57, Appl
Sequence 10, Appl					Sequence 10, Appl
Sequence 10, Appl					Sequence 10, Appl
Sequence 20, Appl					Sequence 20, Appl
Sequence 10, Appl					Sequence 10, Appl
Sequence 15, Appl					Sequence 15, Appl
Sequence 54, Appl					Sequence 54, Appl
Sequence 54, Appl					Sequence 54, Appl
Sequence 87, Appl					Sequence 87, Appl
Sequence 6, Appli					Sequence 6, Appli
Patent No. 5463174					Patent No. 5463174
Sequence 162, App					Sequence 162, App
Sequence 27, Appl					Sequence 27, Appl
Sequence 28, Appl					Sequence 28, Appl
Sequence 9, Appli					Sequence 9, Appli
Sequence 100, App					Sequence 100, App
Sequence 26, Appl					Sequence 26, Appl
Sequence 26, Appl					Sequence 26, Appl

c 28	13.2	62.9	38	4	US-09-614-022-26	Sequence 26, Appl
c 29	13	61.9	23	1	US-08-390-850-363	Sequence 363, App
c 30	13	61.9	23	1	US-08-435-634-363	Sequence 363, App
c 31	13	61.9	31	1	US-08-390-850-93	Sequence 93, Appl
c 32	13	61.9	31	1	US-08-390-850-94	Sequence 94, Appl
c 33	13	61.9	31	1	US-08-390-850-95	Sequence 95, Appl
c 34	13	61.9	31	1	US-08-435-634-93	Sequence 93, Appl
c 35	13	61.9	31	1	US-08-435-634-94	Sequence 94, Appl
c 36	13	61.9	31	1	US-08-435-634-95	Sequence 95, Appl
c 37	13	61.9	34	3	US-09-082-664-2	Sequence 2, Appli
c 38	13	61.9	40	2	US-08-713-815A-6	Sequence 6, Appli
c 39	13	61.9	44	3	US-08-782-480-11	Sequence 11, Appl
c 40	13	61.9	44	4	US-08-954-211-11	Sequence 11, Appl
c 41	13	61.9	44	4	US-09-005-167A-11	Sequence 11, Appl
c 42	13	61.9	44	4	US-09-176-741B-11	Sequence 11, Appl
c 43	13	61.9	45	3	US-08-721-458B-62	Sequence 62, Appl
c 44	12.8	61.0	27	3	US-08-985-162-1581	Sequence 1581, Ap
c 45	12.8	61.0	27	4	US-08-584-040-393	Sequence 393, App

ALIGNMENTS

RESULT 1
US-07-885-689A-7
; Sequence 7, Application US/07885689A
; Patent No. 5366876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; HORMONE USING A SYNTHETIC GENE.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,689A
; FILING DATE: 19-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 377-144P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY:
; LOCATION: 1..45
; OTHER INFORMATION: /label= oligonucleotide

OTHER INFORMATION: /note= "U7 oligonucleotide portion of synthetic
OTHER INFORMATION: BGH gene, Figure 1."
US-07-895-689A-7

Query Match 73.3%; Score 15.4; DB 1; Length 45;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 20
|||||

Db 21 CAGCAGAGTCTTCACCA 37
|||||

RESULT 2

US-08-467-603-35/C
Sequence 35, Application US/08467603
Patent No. 5843672

GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzej
APPLICANT: Bizindauskas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,603
FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549

FILING DATE: 07/999,712

FILING DATE: 31-Dec-92

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-467-603-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGTCTTCATC 19
|||||

Db 24 AGGACGAGGCTTCATC 7
|||||

RESULT 3

US-08-466-793-35/C
Sequence 35, Application US/08466793
Patent No. 5891716

GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzej
APPLICANT: Bizindauskas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/156,549

FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 07/999,712

FILING DATE: 31-Dec-92

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-466-793-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGTCTTCATC 19
|||||

Db 24 AGGACGAGGCTTCATC 7
|||||

RESULT 4

US-08-491-861A-35/C

Sequence 35, Application US/08491861A

Patent No. 5939283

GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.

APPLICANT: Kanieczny, Andrzej

APPLICANT: Bizindauskas, Christine B.

APPLICANT: Brauer, Andrew W.

TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog

TITLE OF INVENTION: Dander and Uses Therefor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

FILE REFERENCE: wsr13885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide corresponding to amino acid
OTHER INFORMATION: sequence set forth in SEQ ID NO:46
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(24)
OTHER INFORMATION: oligonucleotide that corresponds to the conserved
OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:46
US-09-360-545-57

Query Match 67.6%; Score 14.2; DB 4; Length 24;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
DB 24 CAGCAGCAGAGTCTTCAC 6
|||||

RESULT 9
US-09-130-663-10/c
Sequence 10, Application US/09130663A
Patent No. 6020163
GENERAL INFORMATION:
APPLICANT: Konklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer: ZC13270
US-09-130-663-10

Query Match 67.6%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
DB 27 CAGGACAGGGTCTTCATC 9
|||||

RESULT 10
US-09-432-335-10/c
Sequence 10, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
APPLICANT: Konklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335

CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer: ZC13270
US-09-432-335-10

Query Match 67.6%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
DB 27 CAGGACAGGGTCTTCATC 9
|||||

RESULT 11
US-09-254-023B-20
Sequence 20, Application US/09254023B
Patent No. 6225077
GENERAL INFORMATION:
APPLICANT: SCHMIDT, Gunter
THOMPSON, Andrew Hugin
TITLE OF INVENTION: CHARACTERISING DNA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,023B
FILING DATE: 20-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/02403
FILING DATE: 05-SEP-1997
APPLICATION NUMBER: GB 9618544.2
FILING DATE: 05-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 020600-275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-254-023B-20

Query Match 67.6%; Score 14.2; DB 4; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTCATCAT 21
 |||||
 Db 1 GCAGCAGAGTCTTCATCAT 19

RESULT 12

US-09-614-022-10/c
 ; Sequence 10, Application US/09614022
 ; Patent No. 6365716
 ; GENERAL INFORMATION:
 ; APPLICANT: Konklin, Darrell C.
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG
 ; FILE REFERENCE: 97-24
 ; CURRENT APPLICATION NUMBER: US/09/614,022
 ; CURRENT FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 09/130,663
 ; PRIOR FILING DATE: 1998-08-06
 ; PRIOR APPLICATION NUMBER: 60/054,867
 ; PRIOR FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer: 2C13270
 US-09-614-022-10

Query Match 67.6%; Score 14.2; DB 4; Length 30;
 Best Local Similarity 84.2%; Pred. No. 5.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 |||||
 Db 27 CAGGACAGGGTCTTCATC 9

RESULT 13

US-09-256-496-15
 ; Sequence 15, Application US/09256496
 ; Patent No. 5998206
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
 ; FILE REFERENCE: RTS-0056
 ; CURRENT APPLICATION NUMBER: US/09/256,496
 ; CURRENT FILING DATE: 1999-02-23
 ; NUMBER OF SEQ ID NOS: 86
 ; SEQ ID NO 15
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-256-496-15

Query Match 65.7%; Score 13.8; DB 2; Length 18;
 Best Local Similarity 88.2%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCA 17
 |||||
 Db 1 CAGCAGCAGGATCTTCA 17

RESULT 14

US-08-467-603-54/c
 ; Sequence 54, Application US/08467603
 ; Patent No. 5843672
 ; GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
 APPLICANT: Kanieczny, Andrzej
 APPLICANT: Bizindaukas, Christine B.
 APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,603
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/156,549
 FILING DATE:
 APPLICATION NUMBER: 07/999,712
 FILING DATE: 31-Dec-92
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandraouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-0266CP(IPC-048CP)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-467-603-54

Query Match 65.7%; Score 13.8; DB 2; Length 37;
 Best Local Similarity 88.2%; Pred. No. 8.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCAT 18
 |||||
 Db 30 AGGAGCAGGGTCTTCAT 14

RESULT 15

US-08-466-793-54/c
 ; Sequence 54, Application US/08466793
 ; Patent No. 5891716
 ; GENERAL INFORMATION:
 ; APPLICANT: Morgenstern, Jay P.
 ; APPLICANT: Kanieczny, Andrzej
 ; APPLICANT: Bizindaukas, Christine B.
 ; APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-466-793-54

Query Match 65.7%; Score 13.8; DB 2; Length 37;
Best Local Similarity 88.2%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AGCAGCAGAGTCTTCAT 18
||| ||||| ||||| |||||
Db 30 AGGAGCAGGGTCTTCAT 14

Search completed: April 18, 2003, 08:56:37
Job time : 61 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:05:10 ; Search time: 1839 Seconds
(without alignments)
332.332 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21
Sequence: 1 cagcagcagagcttcattcat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rnd.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sv.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
C 1	16.2	77.1	48	6	A76301 Sequence 7
C 2	16.2	77.1	48	6	E01067 DNA sequenc
C 3	15.4	73.3	39	6	A08489 B.taurus ge
C 4	15.4	73.3	39	6	A12568 fragment of
C 5	15.4	73.3	45	6	A05116 Oligonucleo
C 6	15.2	72.4	22	6	AX268965 Sequence
C 7	14.8	70.5	27	6	AX118356 Sequence
C 8	14.8	70.5	31	6	AX070079 Sequence
C 9	14.6	69.5	48	6	A76303 Sequence 9
C 10	14.4	68.6	39	6	A08490 oligonucleo
C 11	14.4	68.6	39	6	A08491 oligonucleo
C 12	14.4	68.6	39	6	A12569 fragment of
C 13	14.4	68.6	39	6	A12570 fragment of
C 14	14.2	67.6	20	6	AR085567 Sequence
C 15	14.2	67.6	30	6	A70102 Sequence 20
C 16	14.2	67.6	30	6	AR148235 Sequence
C 17	14.2	67.6	30	6	AR204084 Sequence
C 18	13.8	65.7	18	6	AR092800 Sequence
C 19	13.8	65.7	31	6	A36373 Sequence 6
C 20	13.8	65.7	37	6	AR070094 Sequence
C 21	13.8	65.7	50	6	AX233374 Sequence
C 22	13.6	64.8	50	6	AX080828 Sequence
C 23	13.6	64.8	50	6	AX403425 Sequence
C 24	13.4	63.8	34	6	AR045234 Sequence
C 25	13.4	63.8	34	6	I52286 Sequence 27
C 26	13.2	62.9	18	6	AR085592 Sequence
C 27	13.2	62.9	23	6	AX262444 Sequence
C 28	13.2	62.9	26	6	AX462235 Sequence
C 29	13.2	62.9	31	6	AX249499 Sequence
C 30	13.2	62.9	32	6	AX339313 Sequence
C 31	13.2	62.9	33	6	A36538 Sequence 79
C 32	13.2	62.9	33	6	AR080171 Sequence
C 33	13.2	62.9	34	6	A93582 Sequence 12
C 34	13.2	62.9	34	6	BD012889 Nucleus 1
C 35	13.2	62.9	34	23	BD008324 Nucleus 1
C 36	13.2	62.9	35	6	AX252822 Sequence
C 37	13.2	62.9	38	6	AR204099 Sequence
C 38	13.2	62.9	47	6	AX114377 Sequence
C 39	13.2	62.9	47	6	AX195012 Sequence
C 40	13	61.9	23	6	A91622 Sequence 14
C 41	13	61.9	23	6	I37350 Sequence 36
C 42	13	61.9	23	6	I94200 Sequence 36
C 43	13	61.9	24	6	E29370 Method for
C 44	13	61.9	27	6	BD013293 DNA compr
C 45	13	61.9	27	23	BD010314 DNA compr

ALIGNMENTS

RESULT 1	A76301	Sequence 7 from Patent WO9319173.	48 bp	DNA	linear	PAT 19-OCT-1999
LOCUS	A76301/c					
DEFINITION	Sequence 7 from Patent WO9319173.					
ACCESSION	A76301					
VERSION	A76301.1	GI:6088388				
KEYWORDS	unidentified.					
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 48)					
AUTHORS	Maegert, H.					
TITLE	DNA CODING FOR APHRODISIN					
JOURNAL	Patent: WO 9319173-A 7 30-SEP-1993;					
	FORSSMANN WOLF GEORG (DE)					

RESULT	3
A08489	
LOCUS	
DEFINITION	A08489 39 bp DNA linear PAT 22-JUL-1993
ACCESSION	B.taurus gene for somatotropin, partial.
VERSION	A08489
KEYWORDS	A08489.1 GI:410773 somatotropin. Bos taurus.
SOURCE	Bos taurus
ORGANISM	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides; Bovidae; Bovinae; Bos. 1 (bases 1 to 39) Harbour/G.C.; Woosterheide,J.G. and Garlick,R.L. Enhanced bioactivity of mammalian somatotropin through selective deamidation Patent: EP 0263206-A 5 13-APR-1988; THE UPJOHN COMPANY Location/Qualifiers 1 .39
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
SOURCE	

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/product="somatotropin"
/protein_id="CAA00787.1"
/db_xref="GI:410774"
/db_xref="SWISS-PROT:P01246"
/translation="LQFLSRVFTNSLV"
8 a 12 c 9 g 10 t

BASE COUNT
ORIGIN

Query Match 73.3%; Score 15.4; DB 6; Length 39;
Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATCA 20
|||||
Db 12 CAGCAGAGTCTTCACCA 28
|||||

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RESULT 4	DNA	linear	PAT 04-JAN-1994
LOCUS			
Al12568			
DEFINITION	39 bp		
fragment of bovine somatotropin.			
ACCESSION			
Al12568			
VERSION			
Al12568.1	GI:488953		
KEYWORDS			
SOURCE			
ORGANISM			
Bos taurus.			
Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;			
Bovidae; Bovinae; Bos.			
Location/Qualifiers			
1..39			
source			
/organism="Bos taurus"			

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BASE COUNT      8 a      13 c      8 g      10 t
ORIGIN

Query Match      73.3%;      Score 15.4;      DB 6;      Length 39;
Best Local Similarity 94.1%;      Pred. No. 1.3e+04;
Matches 16;      Conservative 0;      Mismatches 1;      Indels 0;      Gaps 0;

QY      4      CAGCAGAGTCTTCATCA 20
|||||
Db      12      CAGCAGAGTCTTCACCA 28
|||||

RESULT 5
A05116

```

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ACCESSION A05116
VERSION A05116.1 GI:345003
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
FEATURES
    source
        1..45
            /organism="synthetic construct"
            /db_xref="taxon:32630"
BASE COUNT      8 a      17 c      10 g      10 t
ORIGIN
Query Match      73.3%; Score 15.4; DB 6; Length 45;
Best Local Similarity 94.1%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATCA 20
    ||||| ||||| ||||| ||
Db 21 CAGCAGAGTCTTCACCA 37

RESULT 6
AX268965
LOCUS AX268965
DEFINITION Sequence 46 from Patent WO0175165.
ACCESSION AX268965
VERSION AX268965.1 GI:16541984
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Mcconlogue,L.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,E.
and Bard,F.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 46 11-OCT-2001;
Elan Pharmaceuticals, Inc. (US)
FEATURES
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            /db_xref="taxon:32630"
            /note="forward primer 662F"
BASE COUNT      6 a      8 c      3 g      5 t
ORIGIN

Query Match      72.4%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCA 20
    ||||| ||||| ||||| |||||
Db 2 CAGCACCAGTCTTCATCA 21

RESULT 7
AX118356/c
LOCUS AX118356
DEFINITION Sequence 3479 from Patent WO0129262.
ACCESSION AX118356
VERSION AX118356.1 GI:14035307
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Picoult-Newburg,I. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3479 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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1..27
/note="n = C3 linker"
5 a      8 c      4 g      9 t      1 others
BASE COUNT      5 a      8 c      4 g      9 t      1 others
ORIGIN

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Best Local Similarity 84.2%; Pred. No. 2.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCA 20
    ||||| ||||| ||||| |||||
Db 22 AGCAGCAGTGTGTNCATCA 4

RESULT 8
AR070079/c
LOCUS AR070079
DEFINITION Sequence 35 from patent US 5891716.
ACCESSION AR070079
VERSION AR070079.1 GI:7220967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
AUTHORS Morgenstern,J.P., Konieczny,A., Bizinkauskas,C.B. and Brauer,A.W.
TITLE Allergenic proteins and peptides from dog dander and use therefor
JOURNAL Patent: US 5891716-A 35 06-APR-1999;
FEATURES
    Location/Qualifiers
        source
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BASE COUNT      7 a      13 c      5 g      6 t
ORIGIN

Query Match      70.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 88.9%; Pred. No. 2.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19
    ||||| ||||| ||||| |||||
Db 24 AGGAGCAGGCTTCATC 7

RESULT 9
A76303/c
LOCUS A76303
DEFINITION Sequence 9 from Patent WO9319173.
ACCESSION A76303
VERSION A76303.1 GI:6088390
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
Unclassified.
REFERENCE
AUTHORS Maegert,H.
TITLE DNA CODING FOR APHRODISIN
JOURNAL Patent: WO 9319173-A 9 30-SEP-1993;
FORSSMANN WOLF GEORG (DE)
FEATURES
    Location/Qualifiers
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                /translation="MKVILVLAIVFSLAHA"
BASE COUNT      7 a      8 c      14 g      19 t
ORIGIN
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Query Match 69.5%; Score 14.6; DB 6; Length 48;
Best Local Similarity 81.0%; Pred. No. 3e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
||||| ||||| ||||| |||||
Db 21 CAGCACCAGAGTCTTTACCAT 1

RESULT 10
A08490
LOCUS A08490 39 bp DNA linear PAT 22-JUL-1993
DEFINITION oligonucleotide 3.
ACCESSION A08490
VERSION A08490.1 GI:413472
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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1..39
/organism="synthetic construct"
/db_xref="taxon:32630" 10 t
BASE COUNT 7 a 12 c 10 g 10 t
ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 13
A12570
LOCUS A12570 39 bp DNA linear PAT 04-JAN-1994
DEFINITION fragment of synthetic somatotropin.
ACCESSION A12570
VERSION A12570.1 GI:491410
KEYWORDS
SOURCE
ORGANISM
FEATURES
source
1..39
/organism="synthetic construct"
/db_xref="taxon:32630" 10 t
BASE COUNT 8 a 11 c 10 g 10 t
ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 14
A085567
LOCUS A085567 20 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5981732.
ACCESSION A085567
VERSION A085567.1 GI:10012334
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..20
/organism="unknown"
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BASE COUNT 5 a 8 c 4 g 3 t
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27
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Best Local Similarity 84.2%; Pred. No. 5e+04; Mismatches 0; Indels 3; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 Db 2 CAGCAGCAGAGTCTTCACC 20

RESULT 15

A70102
 LOCUS A70102 30 bp DNA linear PAT 07-MAY-1999
 DEFINITION Sequence 20 from Patent WO9810095.
 ACCESSION A70102
 VERSION A70102.1 GI:4774533
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Thompson, A.H. and Schmidt, G.
 TITLE CHARACTERISING DNA
 JOURNAL Patent: WO 9810095-A 20 12-MAR-1998;
 BRAX GENOMICS LTD (GB)
 FEATURES
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 /db_xref="taxon:32644"
 /organism="unidentified"
 BASE COUNT 5 a 10 c 8 g 7 t
 ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 30;
 Best Local Similarity 84.2%; Pred. No. 4.9e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTCATCAT 21
 Db 1 GCAGCAGAGTCTTCGTCGT 19

Search completed: April 18, 2003, 08:26:54
 Job time : 1855 secs

